

Figure 1 (A)

GAATTCGGCTTCCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCCGGGGCGAGGTATCTTGGCTCACAGGGGA																				79
M	S	S	S	S	W	L	L	L	S	L	V	A	V	T	A	A	Q	S		19
CG	ATG	TCA	AGC	TCT	TCC	TGG	CTC	CTT	CTC	AGC	CTT	GTT	GCT	GTA	ACT	GCT	GCT	CAG	TCC	138
T	I	E	E	Q	A	K	T	F	L	D	K	F	N	H	E	A	E	D	L	39
ACC	ATT	GAG	GAA	CAG	GCC	AAG	ACA	TTT	TTG	GAC	AAG	TTT	AAC	CAC	GAA	GCC	GAA	GAC	CTG	198
F	Y	Q	S	S	L	A	S	W	N	Y	N	T	N	I	T	E	E	N	V	59
TTC	TAT	CAA	AGT	TCA	CTT	GCT	TCT	TGG	AAT	TAT	AAC	ACC	AAT	ATT	ACT	GAA	GAG	AAT	GTC	258
Q	N	M	N	N	A	G	D	K	W	S	A	F	L	K	E	Q	S	T	L	79
CAA	AAC	ATG	AAT	AAT	GCT	GGG	GAC	AAA	TGG	TCT	GCC	TTT	TTA	AAG	GAA	CAG	TCC	ACA	CTT	318
A	Q	M	Y	P	L	Q	E	I	Q	N	L	T	V	K	L	Q	L	Q	A	99
GCC	CAA	ATG	TAT	CCA	CTA	CAA	GAA	ATT	CAG	AAT	CTC	ACA	GTC	AAG	CTT	CAG	CTG	CAG	GCT	378
L	Q	Q	N	G	S	S	V	L	S	E	D	K	S	K	R	L	N	T	I	119
CTT	CAG	CAA	AAT	GGG	TCT	TCA	GTG	CTC	TCA	GAA	GAC	AAG	AGC	AAA	CGG	TTG	AAC	ACA	ATT	438
L	N	T	M	S	T	I	Y	S	T	G	K	V	C	N	P	D	N	P	Q	139
CTA	AAT	ACA	ATG	AGC	ACC	ATC	TAC	AGT	ACT	GGA	AAA	GTT	TGT	AAC	CCA	GAT	AAT	CCA	CAA	498
E	C	L	L	L	E	P	G	L	N	E	I	M	A	N	S	L	D	Y	N	159
GAA	TGC	TTA	TTA	CTT	GAA	CCA	GGT	TTG	AAT	GAA	ATA	ATG	GCA	AAC	AGT	TTA	GAC	TAC	AAT	558
E	R	L	W	A	W	E	S	W	R	S	E	V	G	K	Q	L	R	P	L	179
GAG	AGG	CTC	TGG	GCT	TGG	GAA	AGC	TGG	AGA	TCT	GAG	GTC	GGC	AAG	CAG	CTG	AGG	CCA	TTA	618
Y	E	E	Y	V	V	L	K	N	E	M	A	R	A	N	H	Y	E	D	Y	199
TAT	GAA	GAG	TAT	GTG	GTC	TTG	AAA	AAT	GAG	ATG	GCA	AGA	GCA	AAT	CAT	TAT	GAG	GAC	TAT	678
G	D	Y	W	R	G	D	Y	E	V	N	G	V	D	G	Y	D	Y	S	R	219
GGG	GAT	TAT	TGG	AGA	GGA	GAC	TAT	GAA	GTA	AAT	GGG	GTA	GAT	GGC	TAT	GAC	TAC	AGC	CGC	738
G	Q	L	I	E	D	V	E	H	T	F	E	E	I	K	P	L	Y	E	H	239
GGC	CAG	TTG	ATT	GAA	GAT	GTG	GAA	CAT	ACC	TTT	GAA	GAG	ATT	AAA	CCA	TTA	TAT	GAA	CAT	798
L	H	A	Y	V	R	A	K	L	M	N	A	Y	P	S	Y	I	S	P	I	259
CTT	CAT	GCC	TAT	GTG	AGG	GCA	AAG	TTG	ATG	AAT	GCC	TAT	CCT	TCC	TAT	ATC	AGT	CCA	ATT	858
G	C	L	P	A	H	L	L	G	D	M	W	G	R	F	W	T	N	L	Y	279
GGA	TGC	CTC	CCT	GCT	CAT	TTG	CTT	GGT	GAT	ATG	TGG	GGT	AGA	TTT	TGG	ACA	AAT	CTG	TAC	918
S	L	T	V	P	F	G	Q	K	P	N	I	D	V	T	D	A	M	V	D	299
TCT	TTG	ACA	GTT	CCC	TTT	GGA	CAG	AAA	CCA	AAC	ATA	GAT	GTT	ACT	GAT	GCA	ATG	GTG	GAC	978
Q	A	W	D	A	Q	R	I	F	K	E	A	E	K	F	F	V	S	V	G	319
CAG	GCC	TGG	GAT	GCA	CAG	AGA	ATA	TTC	AAG	GAG	GCC	GAG	AAG	TTC	TTT	GTA	TCT	GTT	GGT	1038
L	P	N	M	T	Q	G	F	W	E	N	S	M	L	T	D	P	G	N	V	339
CTT	CCT	AAT	ATG	ACT	CAA	GGA	TTC	TGG	GAA	AAT	TCC	ATG	CTA	ACG	GAC	CCA	GGA	AAT	GTT	1098
Q	K	A	V	C	H	P	T	A	W	D	L	G	K	G	D	F	R	I	L	359
CAG	AAA	GCA	GTC	TGC	CAT	CCC	ACA	GCT	TGG	GAC	CTG	GGG	AAG	GGC	GAC	TTC	AGG	ATC	CTT	1158
M	C	T	K	V	T	M	D	D	F	L	T	A	H	H	E	M	G	H	I	379
ATG	TGC	ACA	AAG	GTG	ACA	ATG	GAC	GAC	TTC	CTG	ACA	GCT	CAT	CAT	GAG	ATG	GGG	CAT	ATC	1218
Q	Y	D	M	A	Y	A	A	Q	P	F	L	L	R	N	G	A	N	E	G	399
CAG	TAT	GAT	ATG	GCA	TAT	GCT	GCA	CAA	CCT	TTT	CTG	CTA	AGA	AAT	GGA	GCT	AAT	GAA	GGA	1278
F	H	E	A	V	G	E	I	M	S	L	S	A	A	T	P	K	H	L	K	419
TTC	CAT	GAA	GCT	GTT	GGG	GAA	ATC	ATG	TCA	CTT	TCT	GCA	GCC	ACA	CCT	AAG	CAT	TTA	AAA	1338
S	I	G	L	L	S	P	D	F	Q	E	D	N	E	T	E	I	N	F	L	439
TCC	ATT	GGT	CTT	CTG	TCA	CCC	GAT	TTT	CAA	GAA	GAC	AAT	GAA	ACA	GAA	ATA	AAC	TTC	CTG	1398
L	K	Q	A	L	T	I	V	G	T	L	P	F	T	Y	M	L	E	K	W	459
CTC	AAA	CAA	GCA	CTC	ACG	ATT	GTT	GGG	ACT	CTG	CCA	TTT	ACT	TAC	ATG	TTA	GAG	AAG	TGG	1458
R	W	M	V	F	K	G	E	I	P	K	D	Q	W	M	K	K	W	W	E	479
AGG	TGG	ATG	GTC	TTT	AAA	GGG	GAA	ATT	CCC	AAA	GAC	CAG	TGG	ATG	AAA	AAG	TGG	TGG	GAG	1518

09635501-030900

ZBD

Figure 2 (A)

ace-2
 hu-ACET
 mu-ACET
 rb-ACET
 hu-ACE
 mu-ACE
 rat-ACE
 rb-ACE

MGAASGRRGPGLLPLP-----LLLLL-PPQFALALDPGLQPGNFSADDEAGQLFAQSYN
 MGAASGQGRWPLSPPLMLSLVLLLP-SPAPALDPGLQPGNFSADDEAGQLFAESYN
 MGAASGQGRWPLSPPLMLSLVLLLP-SPAPALDPGLQPGNFSADDEAGQLFAESYN
 MGAAPGRRGPRLLRPPPL-LLLLLRPPPAALTDPGLLPDFADEAGARLFASSYN

ace-2
 hu-ACET
 mu-ACET
 rb-ACET
 hu-ACE
 mu-ACE
 rat-ACE
 rb-ACE

SSAEQVLFQSVASWAHDTNITAENARRQEEAALLSQEFAEAWGQKAKELYEPIWQFTD
 SSAEVVMFQSTVASWAHDTNITEENARRQEEAALLSQEFAEAWGQKAKELYEPIWQFTD
 SSAEVVMFQSTASWAHDTNITEENARRQEEAALLSQEFAEAWGQKAKELYEPIWQFTD
 SSAEQVLERSTAASWAHDTNITAENARRQEEAALLSQEFAEAWGRRRLSSMTROGRTSET

ace-2
 hu-ACET
 mu-ACET
 rb-ACET
 hu-ACE
 mu-ACE
 rat-ACE
 rb-ACE

PQLRRIIGAVRTLGSAANLPLAKRQOYNALLSNMSRIYSTAKVCLPNKATCWSLDPDLTN
 SKLRRIIGSIRTLPANLPLAQROQYNALLSNMSRIYSTGKVCFPNKATCWSLDPDLTN
 QKLRIIGSVQTLGPANLPLTQRLQYNALLSNMSRIYSTGKVCFPNKATCWSLDPDLTN
 QSCAGSSGLCAFWPCQAP-GQAAADNSLLSNMSQIYSTGRSASPTLPAAWSLDPDLNN

ace-2
 hu-ACET
 mu-ACET
 rb-ACET
 hu-ACE
 mu-ACE
 rat-ACE
 rb-ACE

ILASSRSYAMLLFAWEGWHNAAGIPLKPLYEDFTALSNEAYKQDGFDTGAYWRSWYNSE
 ILASSRSYAKLLFAWEGWHDAVGIPLKPLYQDFTALSNEAYRQDDFDTGAYWRSWYESP
 ILASSRSYAKVLFWEGWHDAVGIPLRPLYQDFTALSNEAYRQDGFDTGAYWRSWYESP
 ILASSRSYAMLLFAWEGWHNAAGIPLKPLYQDFTALSNEAYRQDGFDTGAYWRSWYDSE

ace-2
 hu-ACET
 mu-ACET
 rb-ACET
 hu-ACE
 mu-ACE
 rat-ACE
 rb-ACE

TFEEDLEHLYQQLPPLYLNLHAFVRRALHRRYGDRYINLRGPIPAHLGDMWAQSWENIY
 SFEESLEHIYHQLPPLYLNLHAFVRRALHRRYGDKYVNLRGPIPAHLGDMWAQSWENIY
 SFEESLEHLYHQVEPLYLNLHAFVRRALHRRYGDKYINLRGPIPAHLGDMWAQSWENIY
 TFEEDLERIYHQLPPLYLNLHAFVRRALHRRYGDRYINLRGPIPAHLGDMWAQSWESIY

ace-2
 hu-ACET
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 rb-ACET
 hu-ACE
 mu-ACE
 rat-ACE
 rb-ACE

DMVVPFDPKPNLDVTSTMLQGGWNATHMFERVAEEFFTSLELSMPPEFWEGSMLEKPADG
 DMVVPFDPKPNLDVTSTMVQKGWNATHMFERVSEEFFTSLELSMPPEFWAESMLEKPTDG
 DMVVPFDPKPNLDVTSTMVQKGWNATHMFERVAEEFFTSLELSMPPEFWAESMLEKPADG
 DMVVPFDPKPNLDVTSTMVQKGWNATHMFERVAEEFFTSLELSMPPEFWAESMLEKPEDG

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REVVCHASAWDFYNRKDERIKQCTRVMTDQLSTVHHMGHIQYYLQYKDLVSLRRGANP
 REVVCHASAWDFYNRKDERIKQCTRVMTDQLSTVHHMGHVQYYLQYKDLVSLRRGANP
 REVVCHASAWDFYNRKDERIKQCTRVMTDQLSTVHHMGHVQYYLQYKDLVSLRRGANP
 REVVCHASAWDFYNRKDERIKQCTQVTMDQLSTVHHMGHVQYYLQYKDPVSLRR-ANP

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hu-ACE
mu-ACE
rat-ACE
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GFHEAIGDVLALS~~V~~STPEHLHKIGLLDRVTNDTESDIN~~Y~~LLKMALEKIAFLPFGYLVDQW
GFHEAIGDVLALS~~V~~STPAHLHKIGLLDHVTNDIESDIN~~Y~~LLKMALEKIAFLPFGYLVDQW
GFHEAIGDVLALS~~V~~STPAHLHKIGLLDRV~~A~~NDIESDIN~~Y~~LLKMALEKIAFLPFGYLVDQW
GFHEAIGDVLALS~~V~~STPAHLHKIGLLDHVTNDTESDIN~~Y~~LLKMALEKIAFLPFGYLVDQW

ace-2
hu-ACET
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rb-ACET
hu-ACE
mu-ACE
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RWGVSGRTPPSRYNEDWYLRTKYQGICPPVTRNETHDAGAKFHPNVTPIRYFVSF
RWGVSGRTPPSRYNEDWYLRTKYQGICPPVARNETHDAGAKFHPNVTPIRYFVSF
RWGVSGRTPPSRYNDWYLRTKYQGICPPVARNETHDAGAKFHIPSVTPPIRYFVSF
RWGVSGRTPSSRYNEDWYLRTKYQGICPPVVRNETHDAGAKFHIPSVTPPIRYFVSF

ace-2
hu-ACET
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mu-ACE
rat-ACE
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-----MGQGWATAGLPSSLFLLLC
-----MGQGWATPGLPSFLELL---LC
-----MGQGWAAPGLPSLILLLLCCGHSLL
VLQFQFHEALCKEAGYEGPLHQCDIYRSTKAGAKLRKVLOAGSSRPWQEVCLKDMVGLDAL
VLQFQFHEALCKEAGHQGPLHQCDIYQSTQAGAKLKQVLOAGCSRWPQEVCLKDLVGSDAL
VLQFQFHEALCKEAGHQGPLHQCDIYQSTKAGAKLQVLOAGCSRWPQEVCLKDLVGSDAL
VLQFQFHEALCKEAGHQGPLHQCDIYQSTRAGAKLRAVLQAGCSRWPQEVCLKDMV7SDAL

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mu-ACE
rat-ACE
rb-ACE

-----MSSSSWLLLSLVAVTAA---QSTIEEQKTF
YGHPLLVPSQEASQQVTVTHGTSSQATTSSQTTTHQATAHQTSQSPNLVLTDEAEASKEV
CGHLLLVLSQVATDHVTANQGITNQATTRSQTTTHQATIDOTTQI-PNLETDEAKADRFV
VPSRVAARRVTVNQGTTSQATTTSKATTSIRATTHQTTAHQTTQS-PNLVLTDEAEASRFV
DAQPLLLKYFQPVTOQLQEONQNGEVLGWPEYQWRPPLPDNYPEG-IDLVTDEAEASKEV
DAKALLEYFQPVSWLEEONQRNGEVLGWPEYQWRPPLPDNYPEG-IDLETDEAKADRFV
DASALMEYFQPVSQWLQEONQRNGEVLGWPEYQWRPPLPDNYPEG-IDLETDEAKANRFV
DAQPLLDYFQPVTOQLQEONERNGEVLGWPEYQWRPPLPNYPPEG-IDLVTDEAEASRFV

ace-2
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rb-ACET
hu-ACE
mu-ACE
rat-ACE
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DKENHEAEDLFYQSSLASWNYNTNITEENVQNMNAGDKW\$AFLKEQSTLAQMYFLOEIQ
 EEYDRTSQVWVNEYAEANWNYNTNITTETSKILLQNMQIANHTLKYGTQARKFDVNQLQ
 EEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTRAKTFDVSNEQ
 EEYDRSFQAVWVNEYAEANWNYNTNITTEASKILLQNMQIANHTLTYGNWARREFDVSNEQ
 EEYDRTSQVWVNEYAEANWNYNTNITTETSKILLQNMQIANHTLKYGTQARKFDVNQLQ
 EEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTRAKTFDVSNEQ
 EEYDRTAKVLWVNEYAEANWHYNTNITIEGSKILLQNKKEVSNHTLKYGTWAKTFDVSNEQ
 EEYDRSFQAVWVNEYAEANWNYNTNITTEASKILLQNMQIANHTLTYGNWARREFDVSNEQ

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mu-ACE
rat-ACE
rb-ACE

NLTVKQLQOALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLN
 NTTIKRIKKVQDLERAALPAQELEEYNKILLDMETTSVATVCHPNG--SCLQLEPDLT
 NSSIKRIKKLQNLDRAVLPPEKEEYNQIILLDMETTSLSNICYTNG--TCMPLEPDLT
 NATSKRIKKVQDLQRAVLVPKELEEYNQIILLDMETIYSVANVCRVDG--SCLQLEPDLT
 NTTIKRIKKVQDLERAALPAQELEEYNKILLDMETTSVATVCHPNG--SCLQLEPDLT
 NSSIKRIKKLQNLDRAVLPPEKEEYNQIILLDMETTSLSNICYTNG--TCMPLEPDLT
 NSTIKRIKKVQNDRAVLPPNELEEYNQIILLDMETTSVANVCYTNG--TCLSLPDLT
 NATSKRIKKVQDLQRAVLVPKELEEYNQIILLMETIYSVANVCRVDG--SCLQLEPDLT

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rat-ACE
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EIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEV
NVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYET
NMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDAGDSWRSLYES
NLMATSRKYDELLWVWTSWRDKVGRAILPYFPHYVEFTNKAARLNGYVDAGDSWRSMYET
NVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYET
NMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDAGDSWRSLYES
NIMATSRKYEELLWVWKSWRDKVGRAILPFFPKYVDFSNKIAKLNGYSDAGDSWRSSYES
NLMATSRKYDELLWVWTSWRDKVGRAILPYFPHYVEFTNKAARLNGYVDAGDSWRSMYET

[illegible]

[illegible]

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TND

LGDK . NEMYLRSSVAYAMRQYFLKVKNQMLFGEDVR RISENFFVTA
 LGWPQYNWAPN-----
 LGWPEYNWAPN-----
 LGWEQYTTWT PN-----
 LGWPQYNWTPN-----
 LGWPEYNWAPN-----
 LGWPEYTTWT PN-----
 LGWPEYTTWT PN-----
 LGWPEYTTWT PN-----
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PKNVSDI I PRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTLGPPNQPPVS WLIVFG
-----SARSE-----GPLPDSGRVS-----FLGLDLD-----AQQARVGQWLLLLFL
-----TARAE-----GSTAESNRVN-----FLGLYLE-----PQQARVGQWLLLLFL
-----SARSE-----GSLPDSGRVN-----FLGMNLD-----AQQARVGQWLLLLFL
-----SARSE-----GPLPDSGRVS-----FLGLDLD-----AQQARVGQWLLLLFL
-----TARAE-----GSTAESNRVN-----FLGLYLE-----PQQARVGQWLLLLFL
-----TARAE-----GSLPESSRVN-----FLGMYLE-----PQQARVGQWLLLLFL
-----SARSE-----GSLPDSGRVN-----FLGMNLD-----AQQARVGQWLLLLFL
      *:*          .  ::*::          ***:          .*:.*:*::*
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VVMGVTVVGIVILIFETGI RDRKKKNKARSGENPYASIDISKGENNPGFQNTDDVQTSFN
GIALLVATLGLSQRLFSIR-HRSLHRHSHG-----PQFGSEVELRHS--
GVALLVATVGLAHRLYNIRNHHSLLRRPHRG-----PQFGSEVELRHS--
GVALLLASLGLTQRLFSIR-YQSLRQPHHG-----PQFGSEVELRHS--
GIALLVATLGLSQRLFSIR-HRSLHRHSHG-----PQFGSEVELRHS--
GVALLVATVGLAHRLYNIRNHHSLLRRPHRG-----PQFGSEVELRHS--
GVALLVATVGLAHRLYNIHNHHSLLRRPHRG-----PQFGSEVELRHS--
GVALLLASLGLTQRLFSIR-YQSLRQPHHG-----PQFGSEVELRHS--
: : : : : * : : : : *

[illegible]

Figure 3 (A)

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

MGAASGSPGLLLPLPLLLLLPPQPALALDPGLQPGNFSAGQLFAQSYNSSAEQV

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

LFQSVAAASWAHDTNITAENARRQEEAALLSQEFAEAWGQKAKELYEPIWQNFTDPQLRRI

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

IGAVRTLGSANLPLAKRQQYNALLSNMSRIYSTAKVCLPNKTATCWSLDPDLTNILASSR

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

SYAMLLFAWEGWHNAAGIPLKPLYEDFTALSNEAYKQDGFTDTGAYWRSWYNSPTFEDDL

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

EHLVQQLLEPLYLNLHAFVRRALHRRYGDRYINLRGPIPAHLLGDMWAQSWENIYDMVVPF

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

PDKPNLDVTSTMLQOGWNATHMFRVAEEFFTSLELSPMPPEFWEGSMLEKPADGREVVCH

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

ASAWDFYNRKDFRIKQCTRVMTDQLSTVHHEMGHIQYYLQYKDLVSLRRGANPGFHEAI

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

GDVLALSVSSTPEHLHKIGLLDRVTNDTESDINYLLKMALEKIAFLPFGYLVDQWRWGVFS

-----MKFHILLLLLV

HUM_tACE
HUM_ACE
DROME_ACE
ace-2
CE_ACE

GRTPPSRYNFDWWYLRTKYQGICPPVTRNETHFDAGAKFHVPNVTPYIRYFVSFVLQFQF

GACLPVFTQEI KPKPELLPADEAPKDPEAVFSEGEPPFELTDALDTPKNGSVPVPEPEPKP

006030" T055E960

Figure 3 (B)

HUM_tACE	-----MGQGWATAGLPSLLFLLLCYGHPLL
HUM_ACE	HEALCKEAGYEGPLHQCDIYRSTKAGAKLRKVLOAGSSRPWQEVLDKMDVGLDALDAQPLL
DROME_ACE	-----
ace-2	-----
CE_ACE	EPEPEPEPKPEPEPSPTPEPEPAIKFDNIESEDYGDVAETAASTQPDDELNTEVIEQLVDT
HUM_tACE	VPSQEASQQVTVTHGTSSQATTSSQTTTHQATAHQTSAQSPNLVTDEAEASKFVEEYDRT
HUM_ACE	KYFQPVTOQLQEQNQNGEVLGWPEYQWHPPLPDNYPEG-IDLVTDEAEASKFVEEYDRT
DROME_ACE	-----MRLFLLALLATLAVTQALVKEEIQAKEYLENLNKE
ace-2	-----MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE
CE_ACE	FLNTGSIASNKTNGKPVFANPVAQALVNSSNYWKTDNLQAPGSIKDEEKLRSLWLAGYEAE
	. * : : :
HUM_tACE	SQVVWNEYAEANWNYNTNITTETSKILLQKNMOIANHTLKYGTQARKFDVNOLQNTTIKR
HUM_ACE	SQVVWNEYAEANWNYNTNITTETSKILLQKNMOIANHTLKYGTQARKFDVNOLQNTTIKR
DROME_ACE	LAKRTNVETEAAWAYGSNITDENEKKKNEISAEKAFMKEVASDTTKFQWRSYQSED LKR
ace-2	AEDLFYQSSSLASWNYNTNITEENVQNMNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKL
CE_ACE	AIKVLREVALSGWRYFNDA SPSLKLALDEAENVLTMFVRSTSMQAKQFDMASVTDEKVMR
	: : * * . : : . : : . . . : : . . . :
HUM_tACE	IIKKVQDLERAALPAQELEEYNKILLDMETTYSVATVCHPNGS---CLQLEPDLTNVMAT
HUM_ACE	IIKKVQDLERAALPAQELEEYNKILLDMETTYSVATVCHPNGS---CLQLEPDLTNVMAT
DROME_ACE	QFKALTKLGYAALPEDDYAELLDTL SAMESNFAKVVC DYKDSTKCDLALDPEIEEVI SK
ace-2	QLQALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQE-CLLLEPGLNEIMAN
CE_ACE	QLGYVSFEGMSALAPSREADYSQAQAALNRDSKDSTICDKDVPPP-CALQKIDMDSIFRN
	: : : * . . : : : * . . . : : : : :
HUM_tACE	SRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYETP----
HUM_ACE	SRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYETP----
DROME_ACE	SRDHEELAYYWREFYDKAGTAVRSQFERYVELNTKAAKLNNFTSGAEAWLDEYEDD----
ace-2	SLDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDG
CE_ACE	EKDASRLQHLWVS YVTAIAKSK-PSYNNIITISNEGAKLNGFANGGAMWRS AFDMS--K
	. . . * : . : : : : * : * : . . . * . : :
HUM_tACE	-----SLEQDLERLFQELQPLYLNLHAYVRRALHRHYG-AQHINLEGPIPAHLLGNMWA
HUM_ACE	-----SLEQDLERLFQELQPLYLNLHAYVRRALHRHYG-AQHINLEGPIPAHLLGNMWA
DROME_ACE	-----TFEQQLEDIFADIRPLYQQIHGYVRFLRKHYG-DAVSETGPIPMHLLGNMWA
ace-2	YDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRALMNAY--PSYISPIGCLPAHLLGDMWG
CE_ACE	VHKA EFDLNKQIDKIYSTIQPFYQLLHAYMRRLAGIYSNPVGLSKDGPIPAHLFGSLDG
	: : : : : : * * * * * * * : : * : * * * * : :
HUM_tACE	QTWSNIYDLVVPFPSA--PSMDTTEAMLKQGWTPRRMFKEADFFFTSLGLLPVPPEFWNK
HUM_ACE	QTWSNIYDLVVPFPSA--PSMDTTEAMLKQGWTPRRMFKEADFFFTSLGLLPVPPEFWNK
DROME_ACE	QQWSEIADIVSPFPEK--PLVDVSAEMEKQAYTPLKMFQMGGDDFFFTSMNLTKLPQDFWDK
ace-2	RFWTNLYSLTVPFQK--PNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFEN
CE_ACE	GDWSAHYEQTKPFEESETP EAMLSAFTNTQNYTTKKMFVTAYRYFKSAGFPHLPKSYWTS
	* : . . * * . : * : . : * . : * * : : . : * . :
HUM_tACE	SMLEKPTDGREVVCHAS-AWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGHIQYFMQYKDL
HUM_ACE	SMLEKPTDGREVVCHAS-AWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGHIQYFMQYKDL
DROME_ACE	SIIEKPTDGRDLVCHAS-AWDFYLIDDVRIKQCTRVTDQDQLETVHHELGHIOYFLQYQHQ
ace-2	SMLTDPGNVQKAVCHPT-AWDLGKG-DFRIILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQ
CE_ACE	SIFAR-VWSKDMICH PAAALDMRAPNDFRVKACAQLGEPDFEQAHSLLVQTYYYQYLYKDQ
	* : : : * * : * * : * : : : : * : : * * :
HUM_tACE	PVALREGANPGFHEAIGDVLALS SVTPKHLHSLNLLSSEGGSD--EHDINFLMKMALDKI
HUM_ACE	PVALREGANPGFHEAIGDVLALS SVTPKHLHSLNLLSSEGGSD--EHDINFLMKMALDKI
DROME_ACE	PFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLLKDYVRDD--EARINQLFLTALDKI
ace-2	PFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI GLLSPDFQEDN-ETEINFLKQALTIV
CE_ACE	SLLFREQASPVITDAIANAF AHLSTNPHYLYSQKLVPSEHLDIKDSVIINKLYKESLESF
	. . * * . : : * : : : : * : : . . . * * : * . :

0053501.080900

Figure 3 (C)

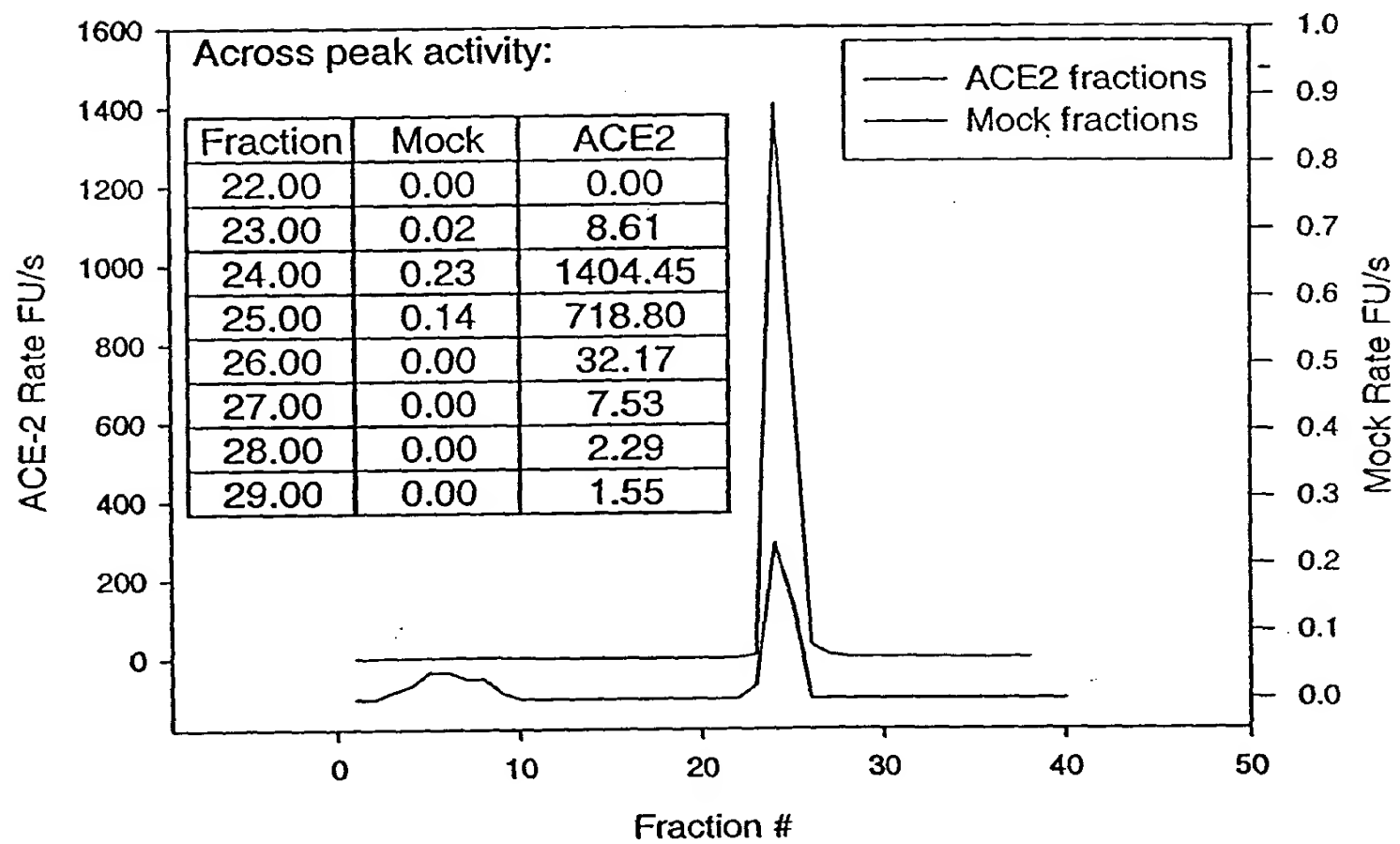
HUM_tACE	AFIPH...QWRWRVFDGSITKENYNQEWWSLRLKYQGL...RTQGDFDPGAKFHIP
HUM_ACE	AFIPFS...QWRWRVFDGSITKENYNQEWWSLRLKYQGL...RTQGDFDPGAKFHIP
DROME_ACE	VFLPFAFTMDKYRWSLFRGEVDKANWNCAFWKLDRDEYSGIEPPVVRSEKDFDAPAKYHIS
ace-2	GTLPFTYMLEKWRWMVFKGEIPKDQWMKKWEMKREIVGVVEPVPHDETYCDPASLFHVS
CE_ACE	TKLPFTIAADNWRYLEFDGTVPKNKLNDRWWEIRNKYEGVRSPPYNTSNLDALIHNSVS
	:*: :*: :* * : * : :*: : * : *
HUM_tACE	-SSVPYIRYFVSFIIQFQFHEALCQAAGHTG-----PLHKCDIYQSKEAGQRLATAMKL
HUM_ACE	-SSVPYIRYFVSFIIQFQFHEALCQAAGHTG-----PLHKCDIYQSKEAGQRLATAMKL
DROME_ACE	-ADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELPLDNCDIYGSARAGAAFHNMLSM
ace-2	-NDYSFIRYTRTLYQFQFQALCQAAGHTG-----PLHKCDISNSTEAGQKLFNMLRL
CE_ACE	QVHSPATRTLISYVLKFQILKALCQRELFWL-----SEGCILSEDTT---EKLRETMKL
	* :*: :* : *
HUM_tACE	GFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLR TEN-----
HUM_ACE	GFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLR TEN-----
DROME_ACE	GASKPWPDALEAFNGERIMSGKALAEYFEPLRVWLEAEN-----
ace-2	GKSEPWTALLENVVGAKNMNVRPLNLYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKV
CE_ACE	GSSITWLKALEMISGKGELDAQPLLEYEPLINWLRNTN-----
	* * . * *: : . * : : . : *: : * * . *
HUM_tACE	-ELHGEKLGWPQYNWTPNSAR-----
HUM_ACE	-ELHGEKLGWPQYNWTPNSAR-----
DROME_ACE	-IKNVHIGWTTSNKCVSS-----
ace-2	RISLKSALGDKAYEWNNDNEMYLFSSVAYAMRQYFLKVKNQMILEGEEDVRVANLKPRIS
CE_ACE	-EIDQVVVGWDGEGTPFTVEEIPKTRQPGDGGNGLPSEDRVAFPGGE-----
	: *
HUM_tACE	-----SEGPLPDSGRVSFLGLDLDAQQARVG-----Q
HUM_ACE	-----SEGPLPDSGRVSFLGLDLDAQQARVG-----Q
DROME_ACE	-----
ace-2	FNFFVTAPKNVSDIIPRTEVEKAI RMSRSRINDAFRLNDNSLEFLGIQPTLGPPNQPPVS
CE_ACE	-----CVNGQECLLD SHCNGTICVCNDGLYTL EIGNTFN---CVPGN
HUM_tACE	WLLLFLGIALLVATLGLSQR LFS-IRHR-----SLHRHSHGPQFGSEVE
HUM_ACE	WLLLFLGIALLVATLGLSQR LFS-IRHR-----SLHRHSHGPQFGSEVE
DROME_ACE	-----
ace-2	<u>IWLIVFGVVMGVIVVGIVILIFTGI</u> RDRKKKNKARS GENPYASIDISKGENNPGFQNTDD
CE_ACE	PADSGFGDGKGGVLVIGLFNNEVTTPEPSAEPEP--TAKTTTKMPPRVRAATSPFSLYLTV
HUM_tACE	LRHS----
HUM_ACE	LRHS----
DROME_ACE	-----
ace-2	VQTSFN--
CE_ACE	LLIIYFAL

TMD

00635501 080900

Figure 4

ACE-2 Fractions: Real vs Mocks



Figures

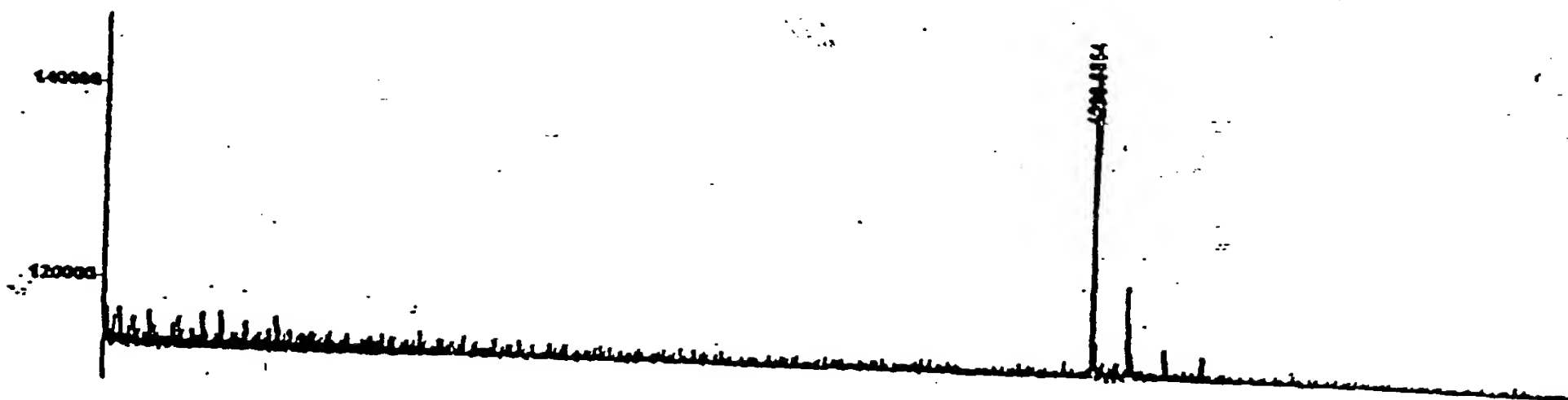


FIGURE 5A

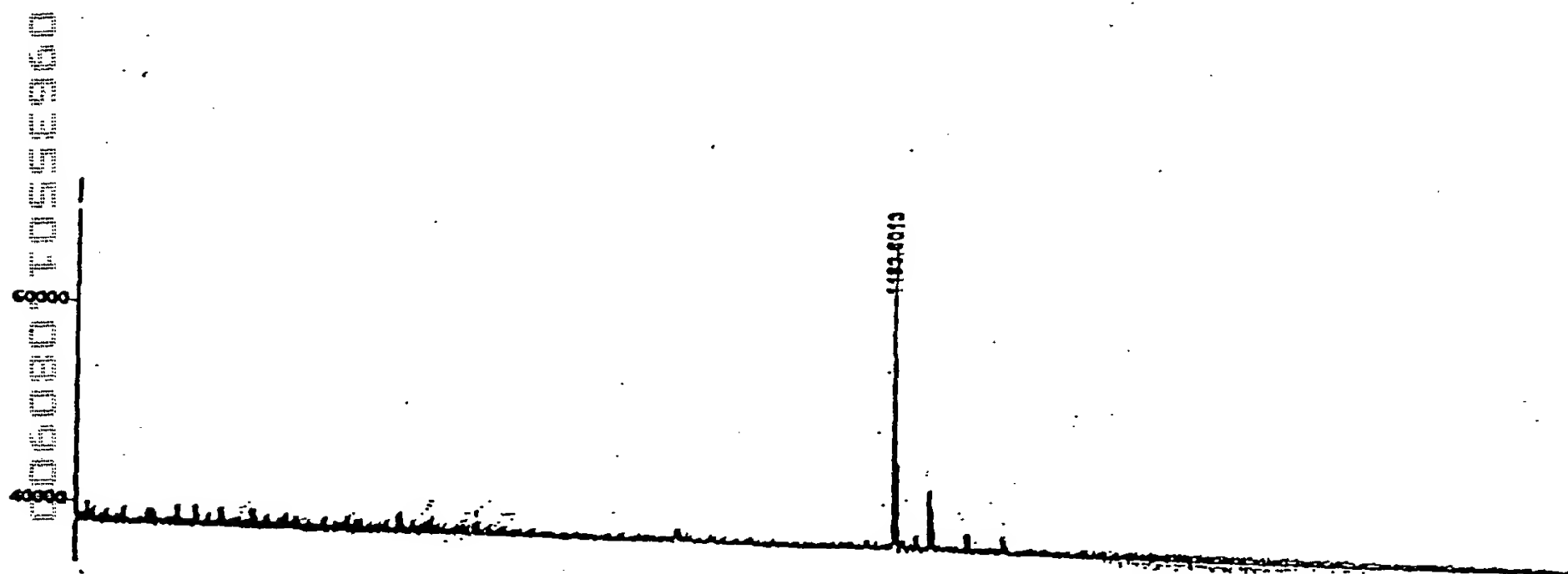


FIGURE 5B

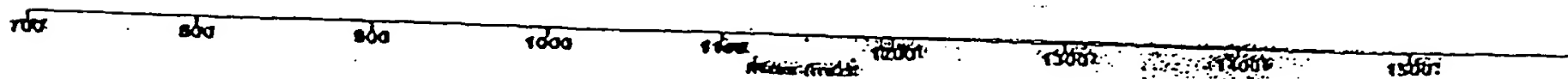


Figure 6

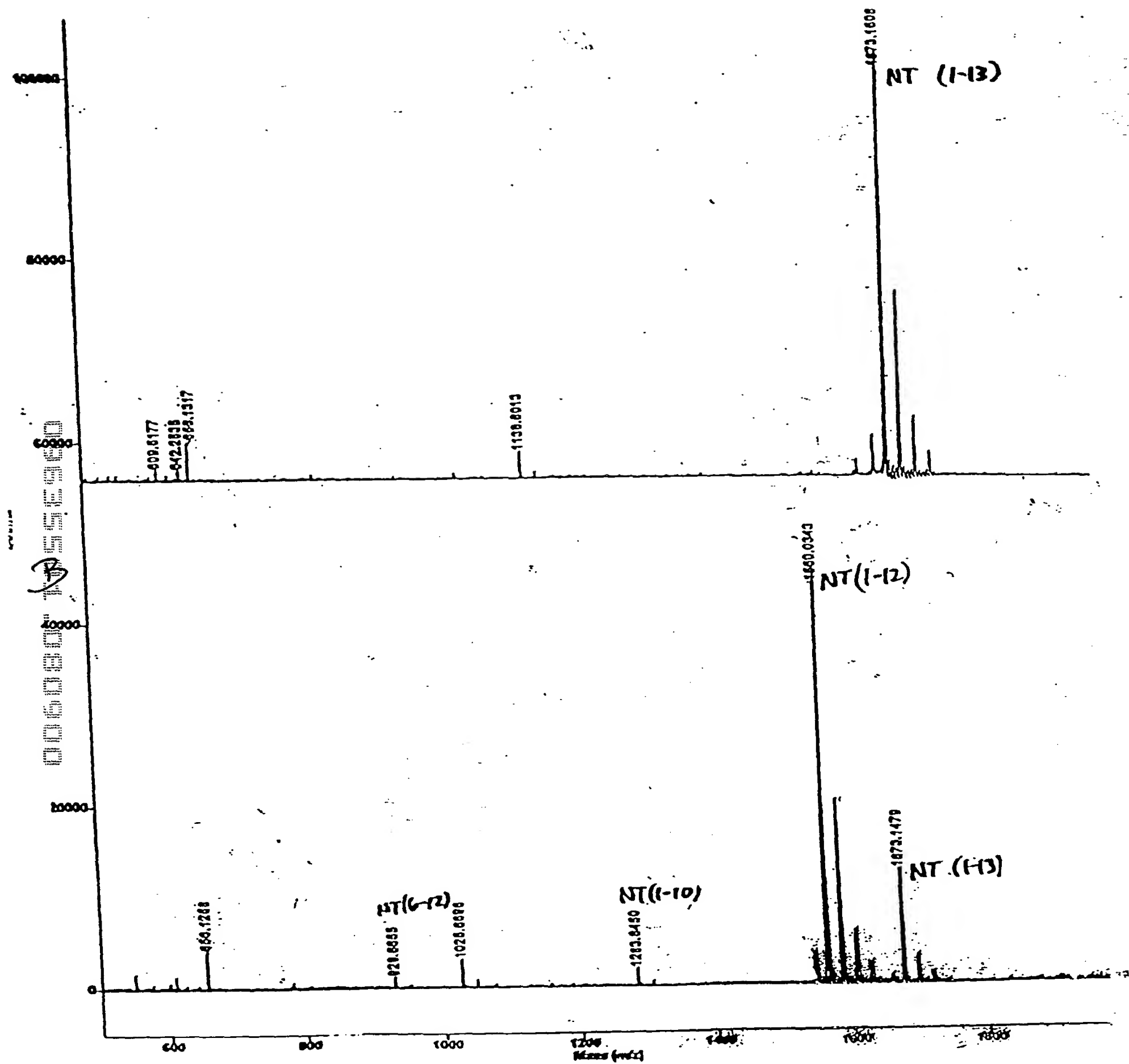


FIGURE 6

Figure 7.

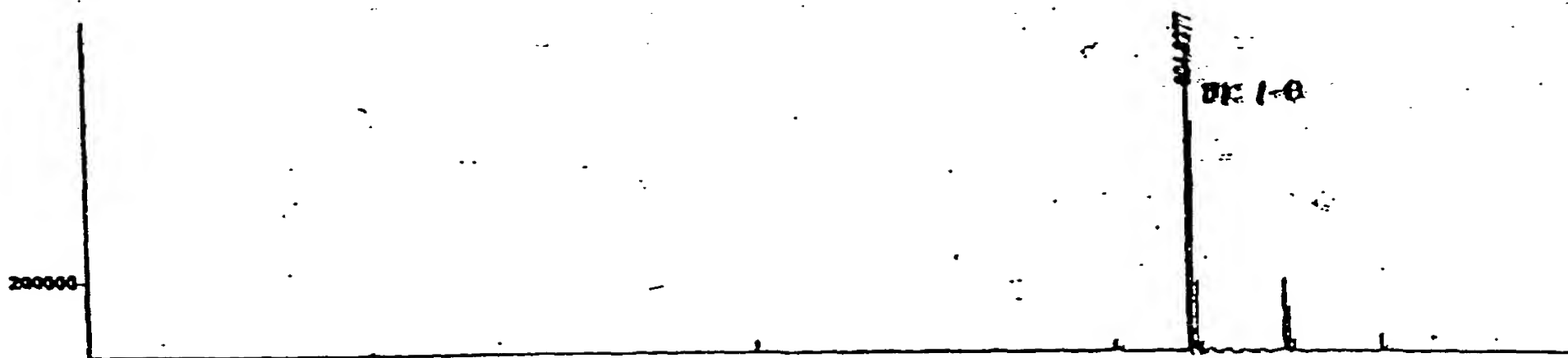


FIGURE 7A

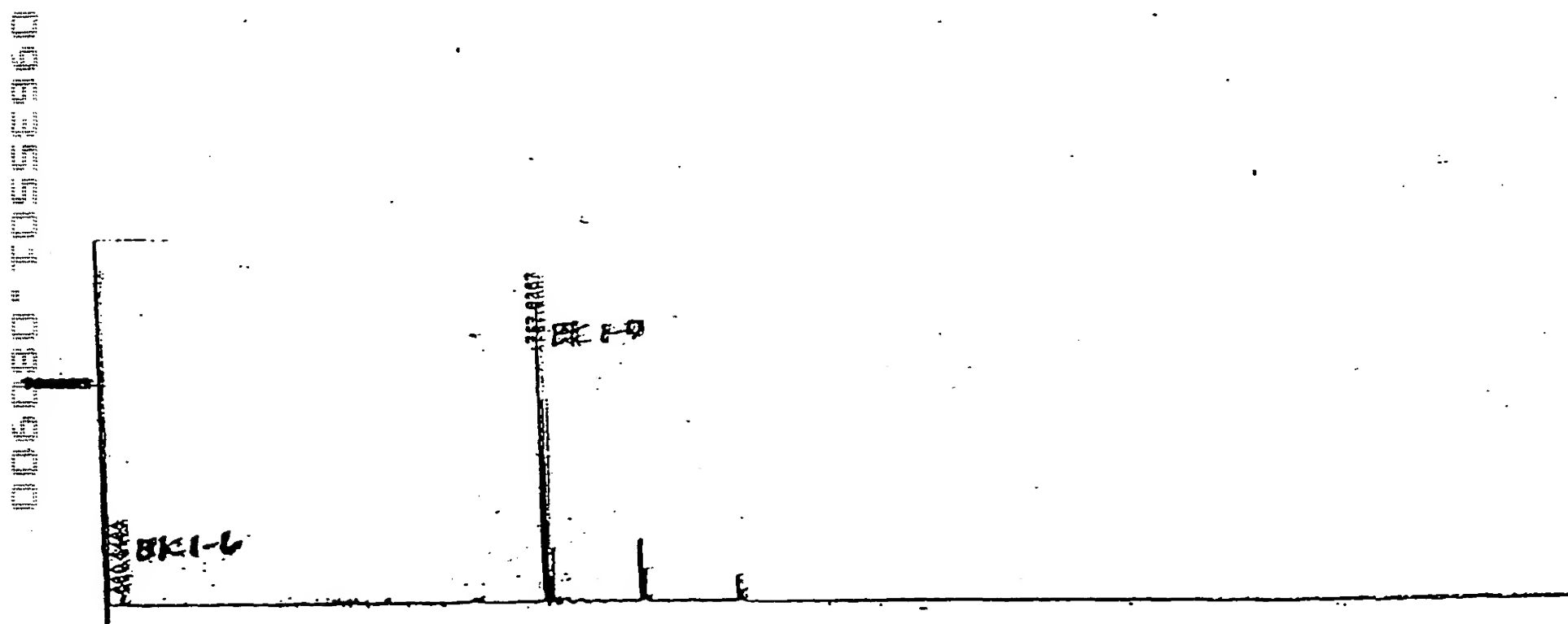


FIGURE 7B

700 750 800 850 900 950

Angiotensin I conversion to products

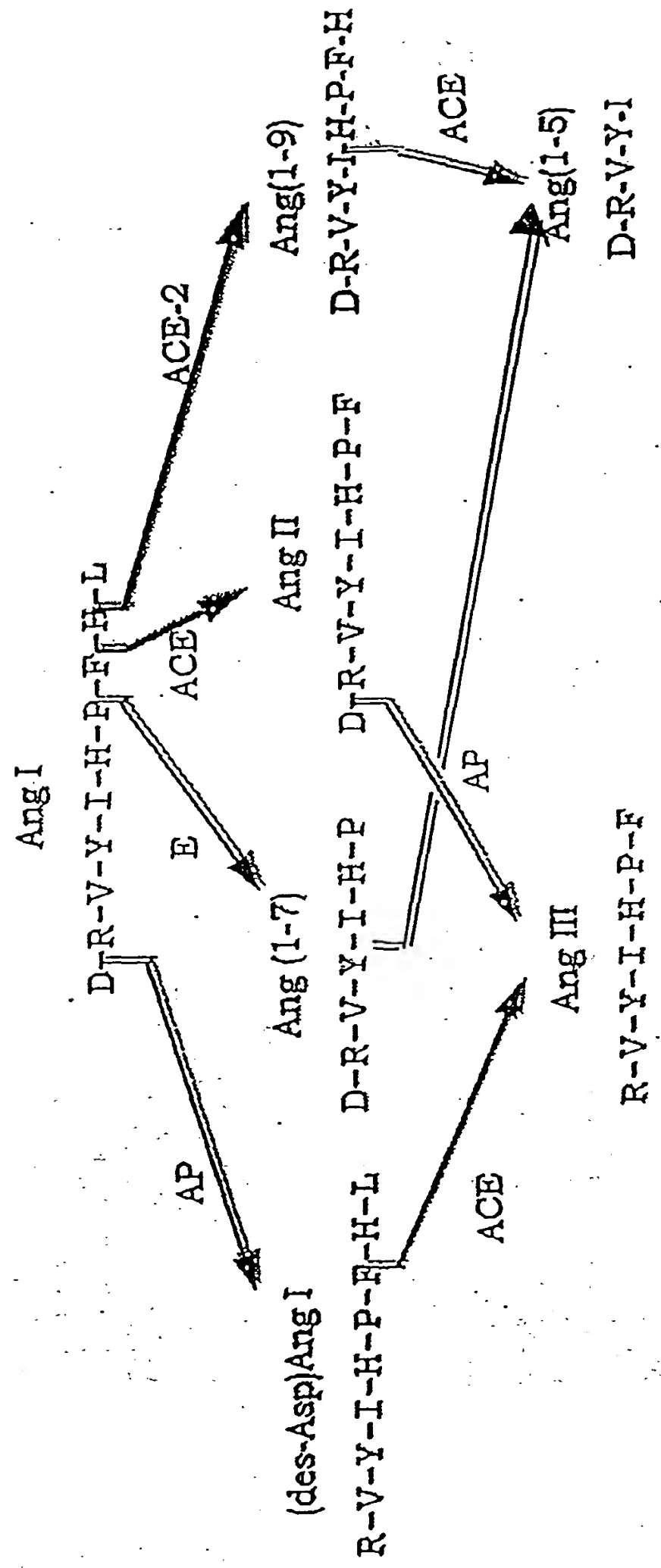
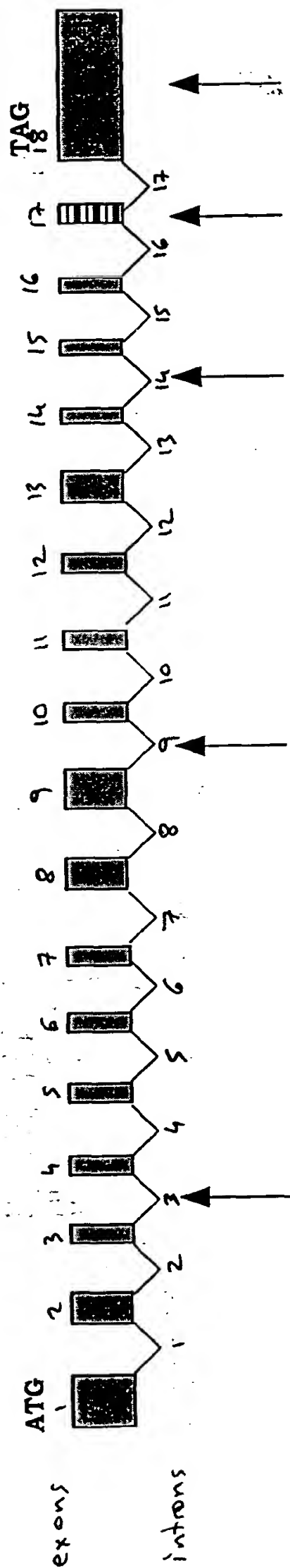


Figure 8

ACE Homologue VARIANTS



ASN → ASP

5 bp insertion
(CTTAT)

G → A

T → G

G → T

0.016

0.250

0.396

0.010

0.005

Figure 9A

[illegible]

GAATTCGGCTTCCATCCTAATACGACTCACTATAGGCTCGAGCGGCCGCCCGGGCCAGGTATCTTTGGCTCACAGGGGACGATGTCAAAC
CTCTTCCTGGCTCCTCTCAGCCTTGTTGCTGTAACCTGCTGCTCAGTCCACCATTTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAAAC
CACGAAGCCGAAGACCTGTTCTATCAAAGTTCACITTCCTTGGAAATTATAACACCAATATTACTGAAGAGAATGTCCAAAAACAT /
GAATAATGCTGGGACAAATGGTCTGCCCTTTTAAAGGAACAGTCCACACTGCC
CAAATGTATCCACTACAAGAAATTCAGAAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGTCTCTCAGAA
GACAAGAGCAAAACGG / TTGAACACAATTCATAAT
ACAATGAGCACCATCTACAGTACTGGAAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACCCAGG L
TTTGAATGAAATAATGGCAACACAGTTTAGACTACAATGAGAGGCTCTGGGC
TTGGGAAAGCTGGAGATCTGAGTCTGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGCTTGAAAAATGAGATGGCAAGAGCA
ATC / ATTATGAGGACTATGGGATTATTGGAGAGGAG
ACTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCCGGCCAGTTGATTGAAGATGTGGAACATACCTTTGAAGAG /
ATTAACCAATTATAGAATCTTCCTATGCTCCCTATGTGAGGGC
AAAGTTGATGAATGCCTATCTTCCTATATCAGTCCAAATGGATGCTCCCTGCTCATTTGCTTGG /
TGATATGTGGGTAGATTTTGGACAAATCTGACTCTTTGACAGTTCCTCTTGGACAGAAA
CCAAACATAGATTTACTGATGCAATGGTGGACCAG / GCCTGGGATGCACAGAGAAATATT
CAAGGAGCCGAGAAATCTTTGTATCTGTGGTCTTCCTAATATGACTCAAGGATTCTGGGAAAAATCCATGCTAAAGGCCAGGAA
TGTTCAGAAAGCAGTCTGCCATCCACAGCTTGGGACCTGGG /
GAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAATGGACGACTTCCTG
ACAGCTCATGATGATGGGCATATCCAGTATGATATGGCATATGCTGCACAACCTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC
CATGAAGCTGTTGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAATCCATTTGCTCTCACCCGATTTCAAGAAG
ACAATG L AACAGAAATAAACTTCTGCTCAAAACAGCACTCACGATTTGTGGGACTCTGCCATTTACTTA
CATGTTAGAGAAATGGAAGTGGATGGTCTTTAAAGGGGAAATTCCTCAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAG /
CGAGAGATAGTTGGGTGGTGGAACTGTGCCCCATGATGAA
CATACTGTGACCCCGCATCTCTGTTCATGTTTCTAATGATTACTCATTCTCG / ATATTACA
CAAGGACCTTTACCAATTCAGTTTCAAGAAAGCACCTTTGTCAAGCAGCTAAACATGAAGGCCCT
CTGCACAAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAACTG /
TTCAATATGCTGAGGCTTGGAAAAATCAGAACCTTGACCTAGCACTTGGAAAAATGTTGTAGGAGCAAGAACATGAATGTAAAGGCCACT
GCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAGAAATCTTTTGTGGATGGAGTACCGACTGGAGTCC /
ATATGCAGACCAAAAGCATCAAAGTGAGGATAAG
CCTAAATCAGCTCTTGAGATAAAGC L ATATGAATGGAACGACAATGAAATGTACC
TGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTAAAGTAAAAAATCAGATGATTCITTTTGGG /
GAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGATCTCCTTTAATTCCTT
GTCAGTGCACCTAAATAATGTGTCTGATATCATTCCTAGAACTGAGTTGAAAGGCCATCAGG /
ATGTCCCGGAGCCGTATCAATGATGCTTTCGCTGTAATGACAACAGCTAGAGTTTCTGGG
GATACAGCCAACACTTGAGCCTCTTAACCAGCCCTGTTTCCATATGCTGATTTTGGAGTTGTGATGGGAGTGATAGTGGTTGG
CAATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAG /
AAAAATAAGCAAGAGTGGAGAAAAATCCTTATGCTCCATCGATATTAGCAAAAGGA
GAAATAATCCAGGATCCAAACACACTGATGATGTTTCAGACCTCCTTTTAGAAAAATCTATGTTTTCTCTTGAGGTGATTTTGTGTGATG
TAAATGTTAATTTCAATGATAGAAAAATATAGATGATAAGATATCAATTAATGTCAAAACTATGACTCTGTCAGAAAAAATAATGTCCAG
AAGACAACATGCCCCAGGATAGGACATCTGATTGACATTTTCAAGTATTTATTTCTGTCTGGAATTTGACTTCTGTTCTTTCTTAA
TAAGGATTTGTATTAGAGTATATTAGGAAAGTGTGATTTGGTCTCACAGGCTGTTCCAGGGATAATCTAAATGTAATGTCTGTGAAAT
TCTGAAGTTGAAAACAAGGATATATCATTTGGAGCAAGTGTGGATCTTGTATGGAAATATGGATGGATCACTGTGAAGCACAGTGCCTGG
GAATCGGTGTAGTGCAGGATTGAGATGGCATGCGATTAGCTCACITTCATTAAATCCATTTGTCAAGGATGACATGCTTTCTTCACAGTA
ACTCAGTTCAAGTACTATGATGATTTCCCTACAGTGAATGTTGGAAATCGATCATGCTTTCTTCAAGGTTGACAGGTTCTAAAGAGAGAGAAAT
CCAGGGAACAGGTAGAGGACATGCTTTTTCACCTCCAGGTTGCTTGATCAACATCTCCCTGACAACACAAAACTAGAGCCAGGGGCT
CCGTGAACCTCCAGAGCATGCTGTATAGAACTCATTTCTACTGTTCTAAGTGTGGAGTGAATGGAAATTCCAACTGTATGTTCCACCT
CTGAAGTGGGTACCCAGTCTCTTAAATCTTTTGTATTGTCTCACAGTGTGTGAGCAGTGTGAGCAAAAGCACACTCAATAAATGCTA
GATTTACACACTC / AAAAAAATAAAAAAGGGGGCCGC

G - A Intronic
3a/3b

5 bp insertion (CTTAT)
Intronic
9a/9b

I - G Intronic
14a/14b

A - G ASN - ASP
17c/17d

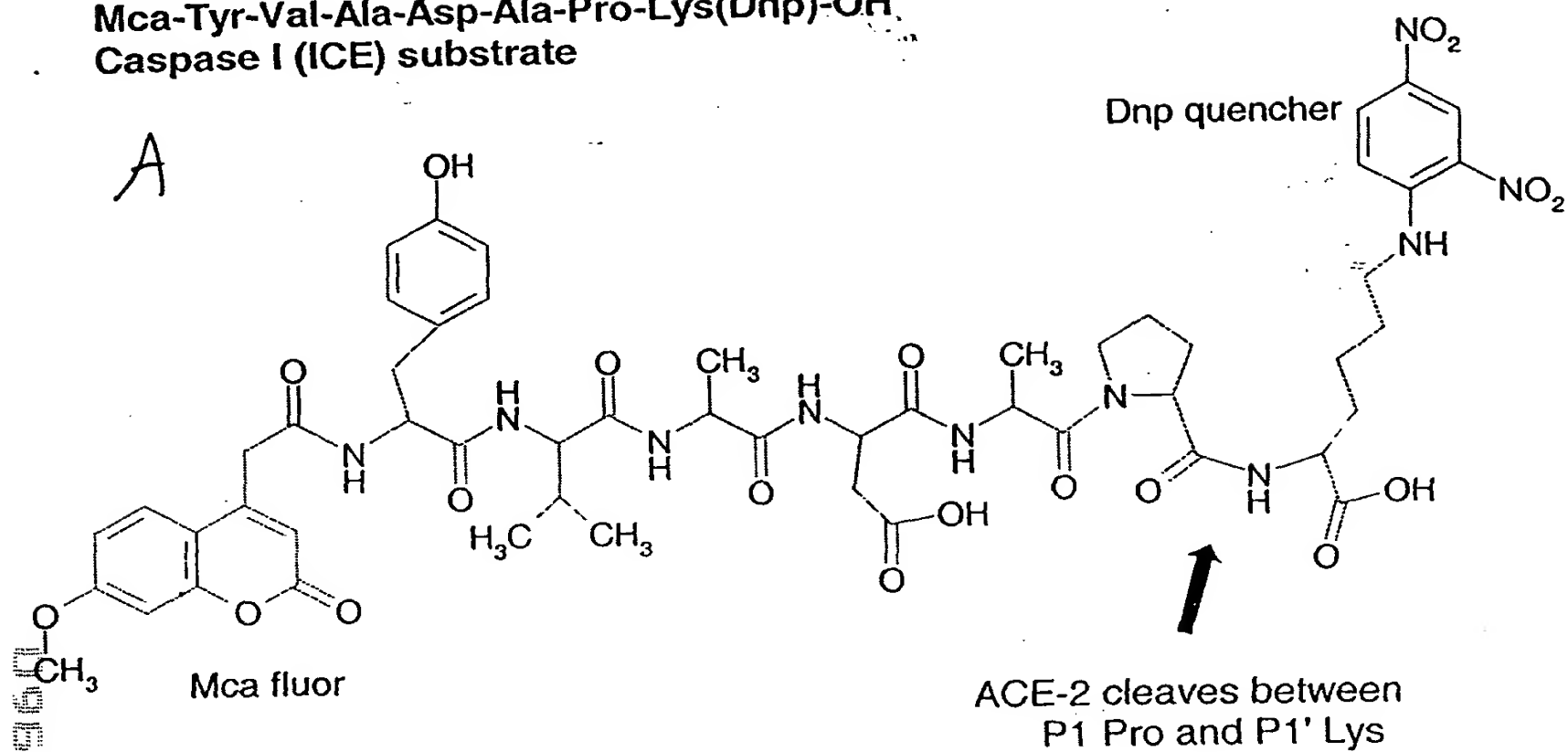
G-T 3'UTR
18e/18f

Figure 9B

Figure 10

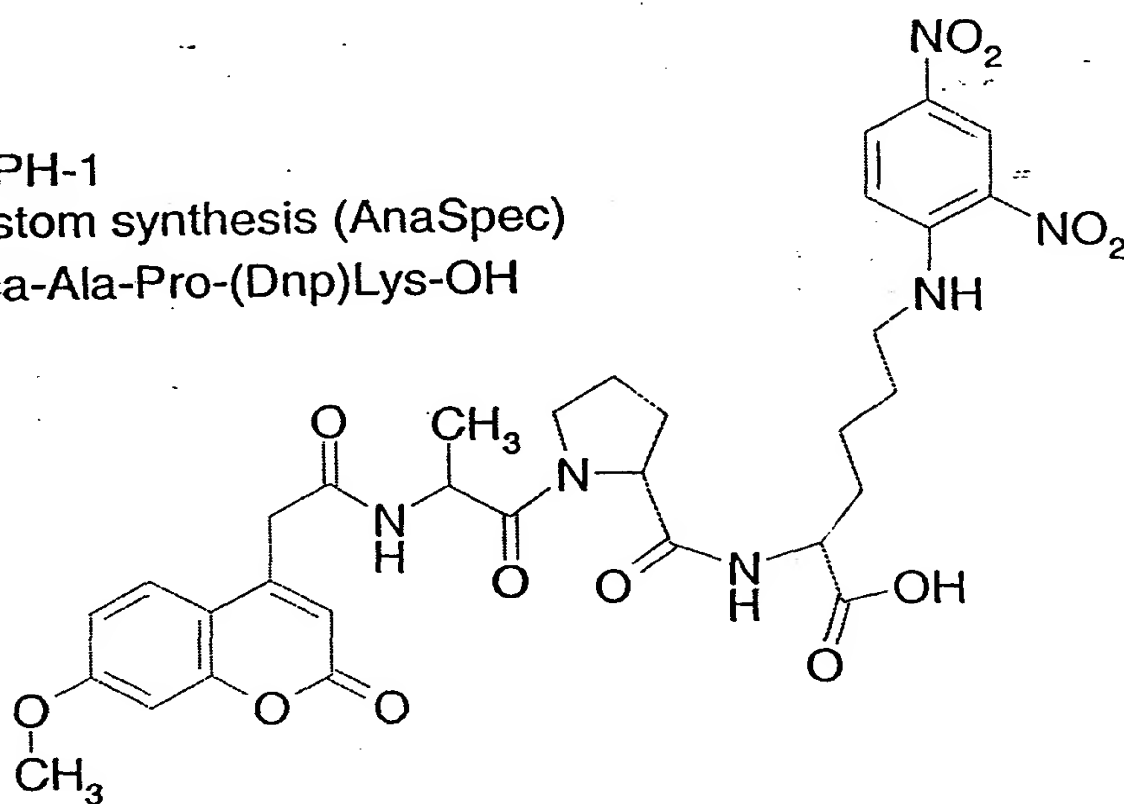
Bachem M-2195
Mca-Tyr-Val-Ala-Asp-Ala-Pro-Lys(Dnp)-OH
Caspase I (ICE) substrate

A

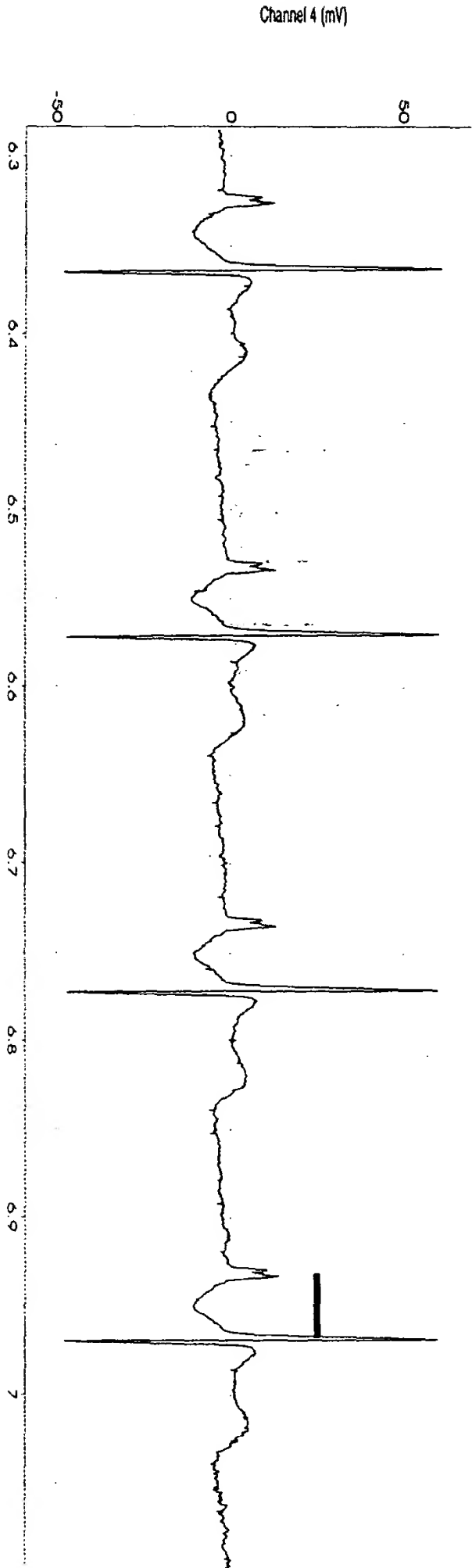


B

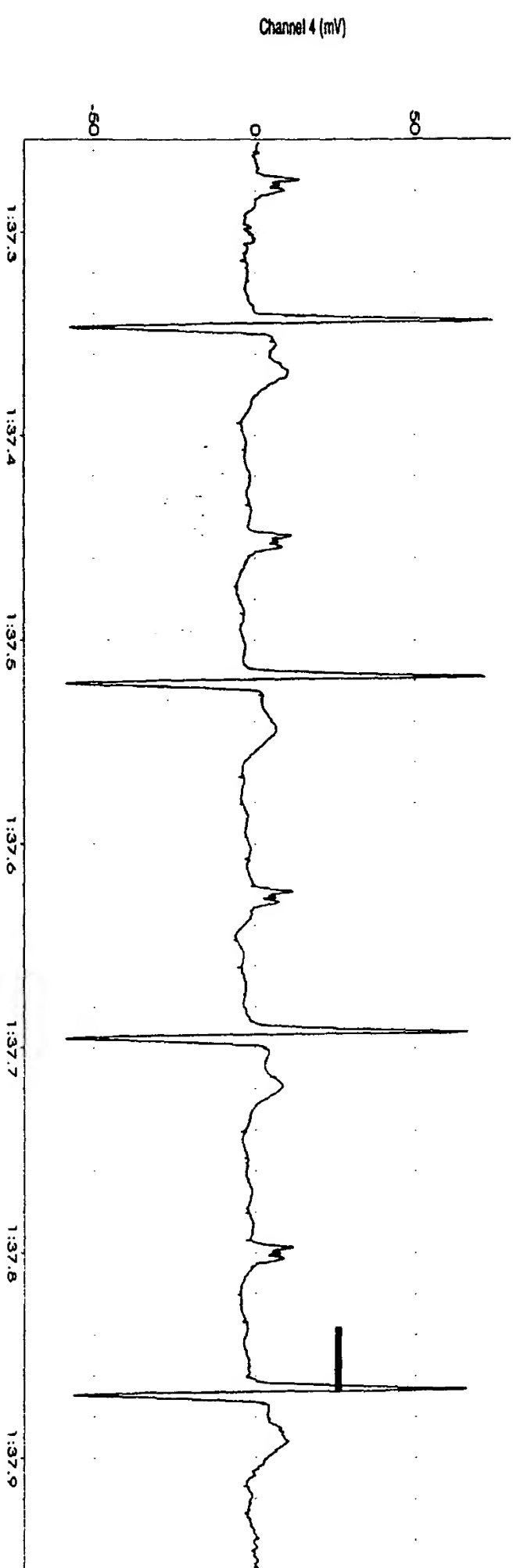
MIPH-1
custom synthesis (AnaSpec)
Mca-Ala-Pro-(Dnp)Lys-OH



Mouse Surface EKG in WT and ACE2 TG Mice



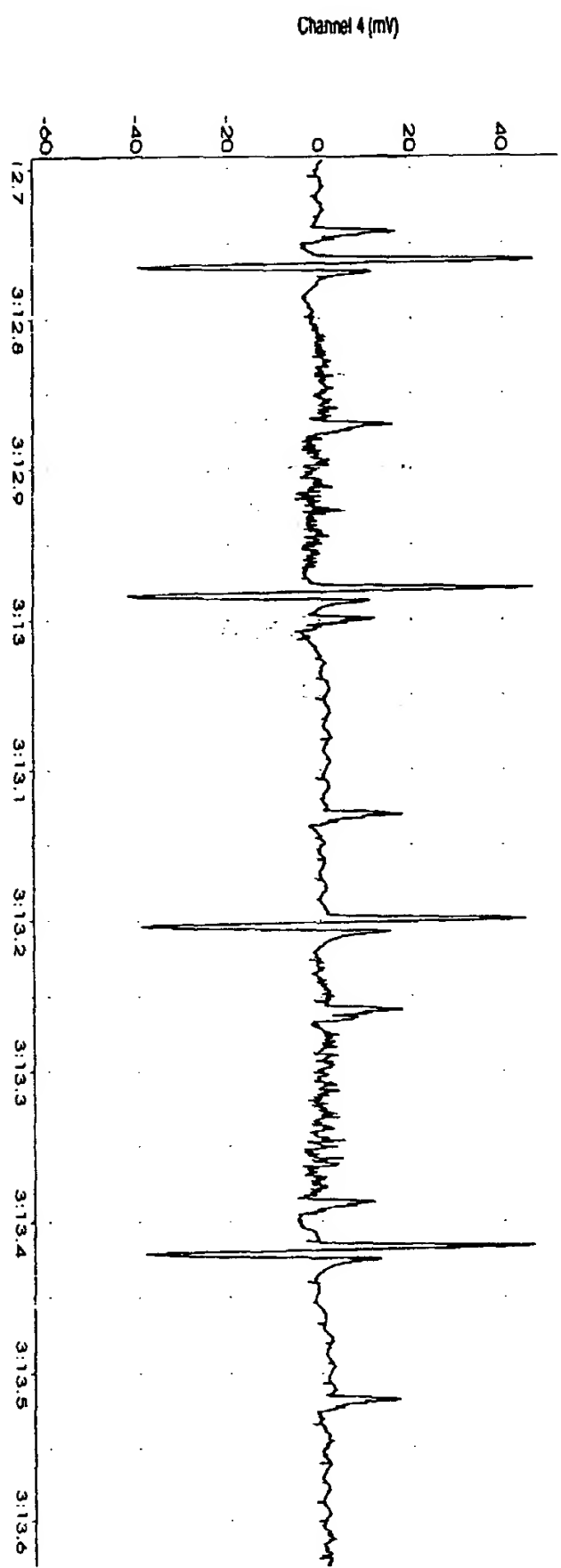
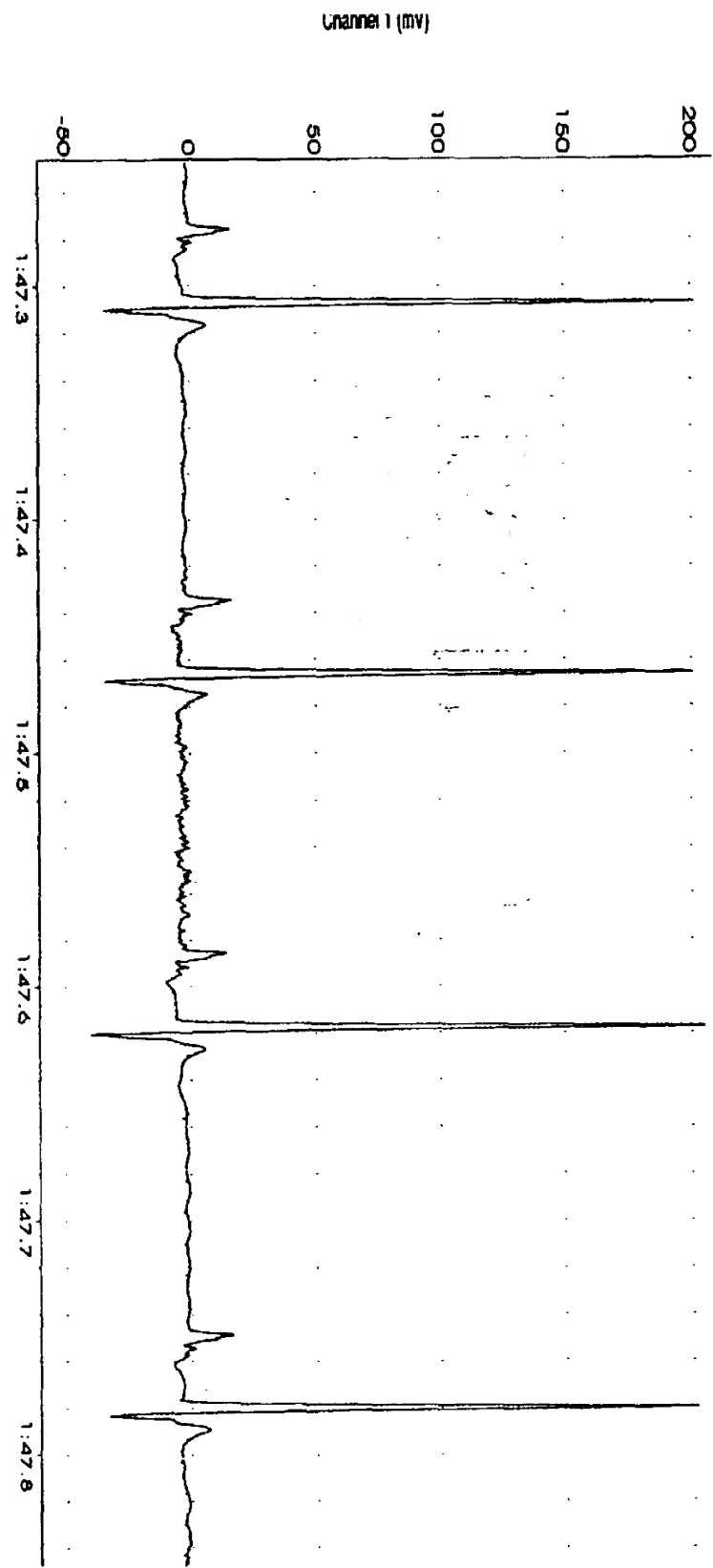
WT (3 day)



TG (3 day)

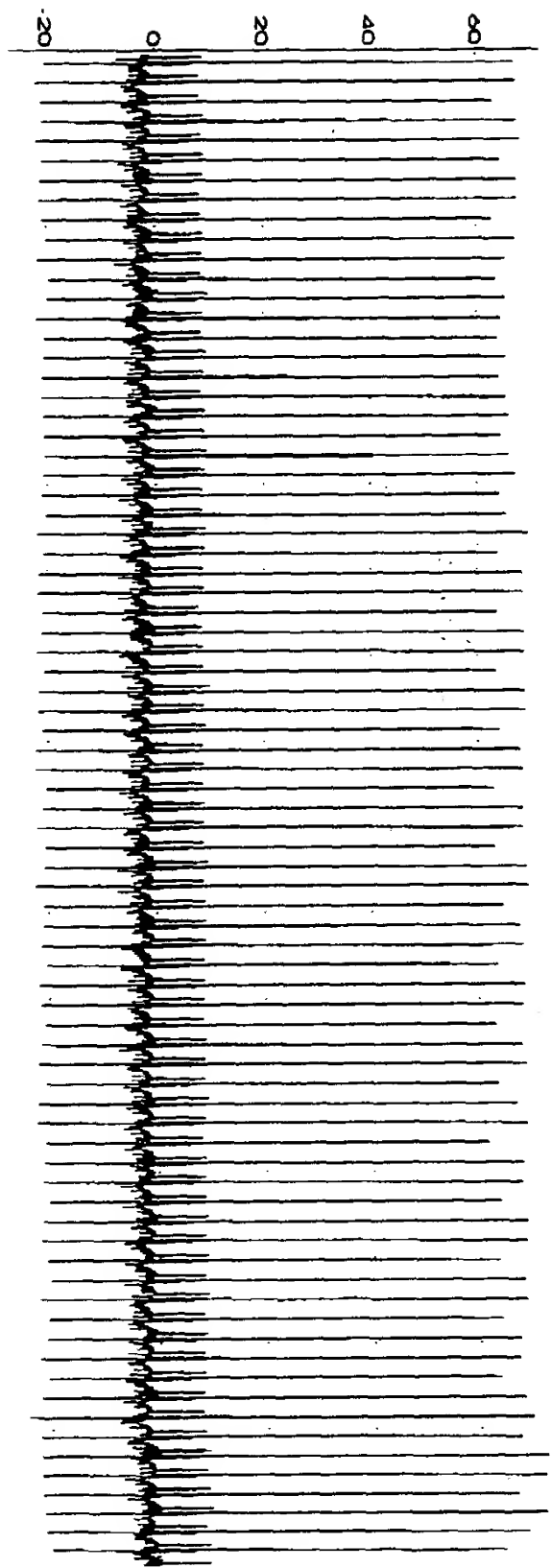
096355
Figure 11A

Mouse Surface EKG in WT and ACE2 TG Mice

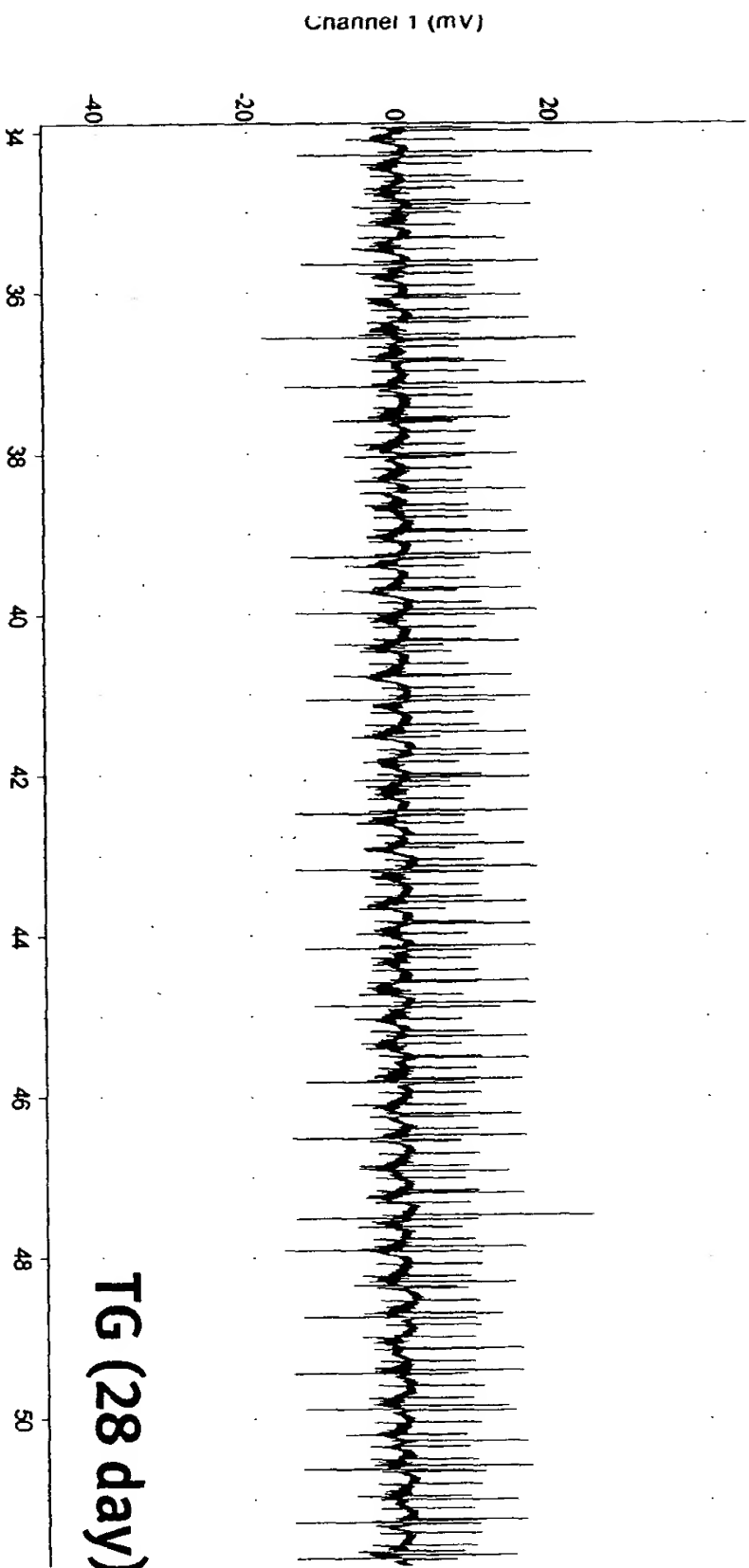
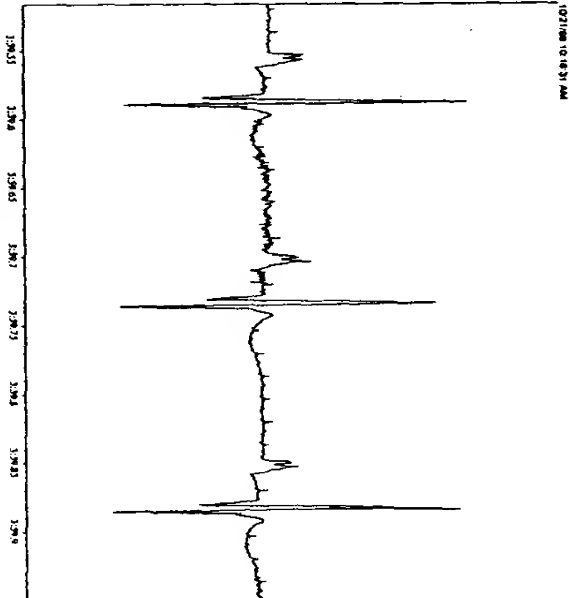


096 Figure 4B

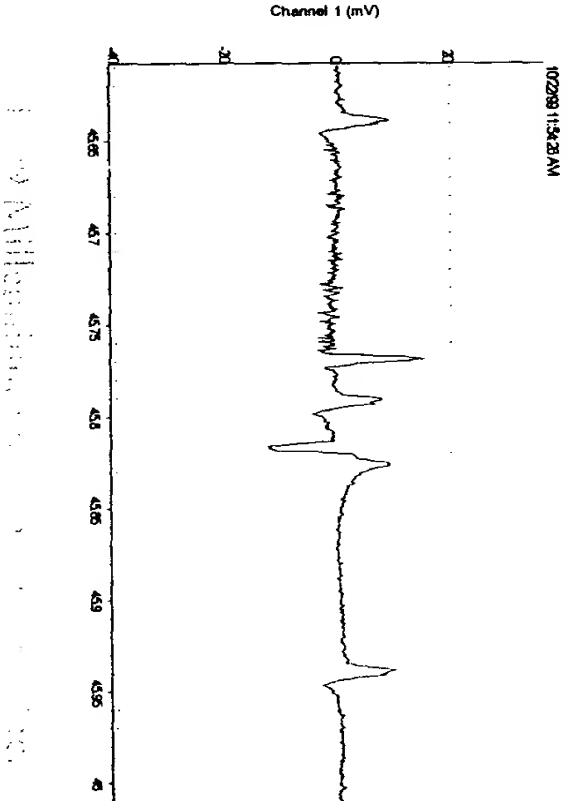
Mouse Surface EKG in WT and ACE2 TG Mice



WT (28 day)



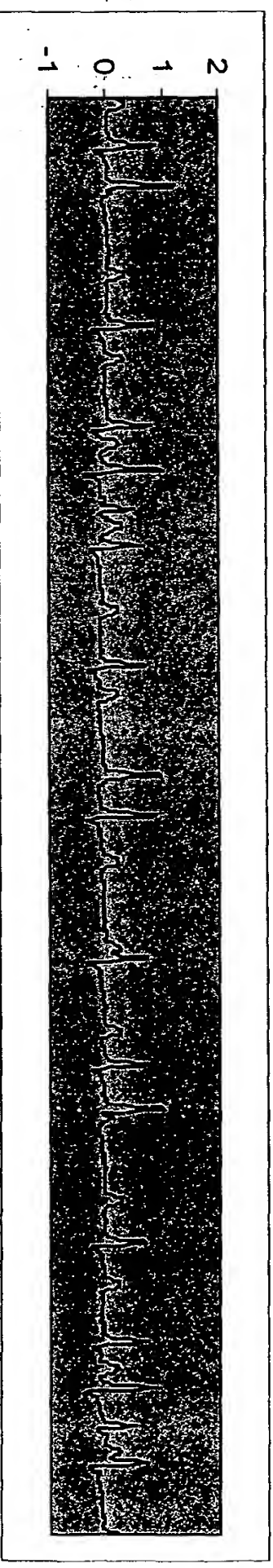
TG (28 day)



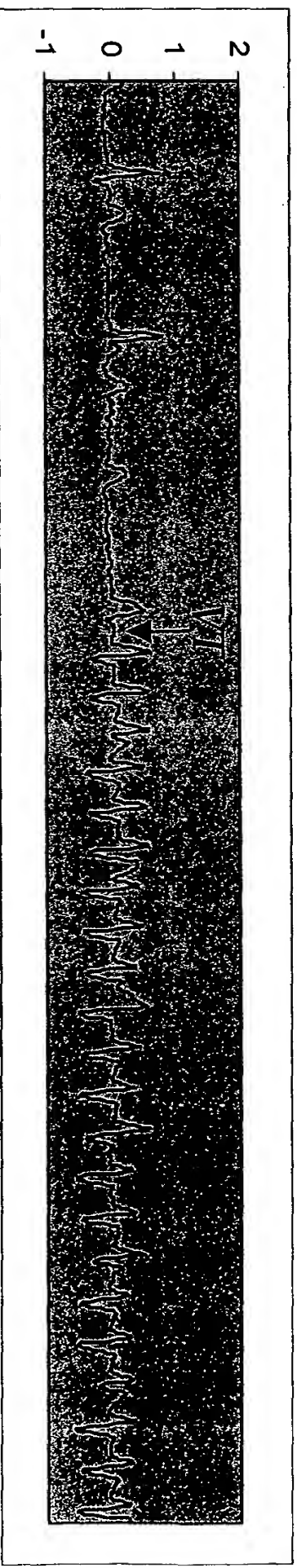
0963503
FIGURE 11C

Sudden Cardiac Death in ACE-2 TG Mice

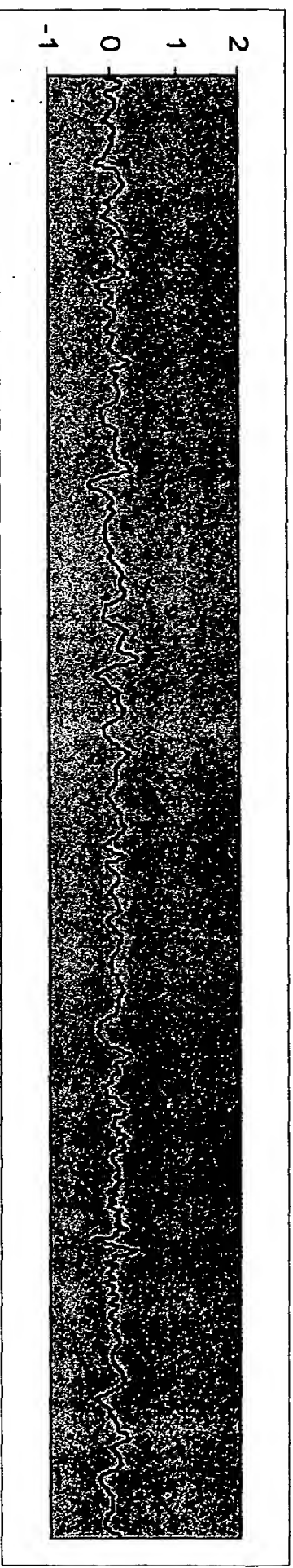
3⁰ Heart Block



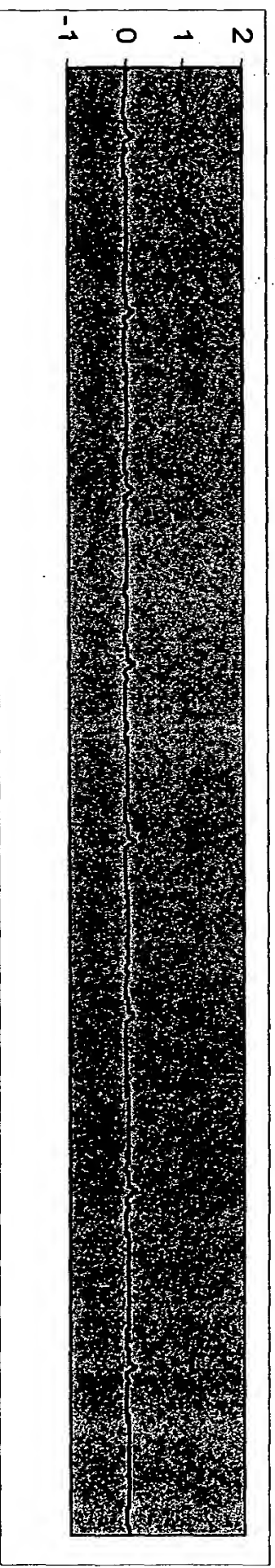
Ventricular
Tachycardia



Ventricular
Fibrillation



Asystole



ACE HOMOLOGUE VARIANTS

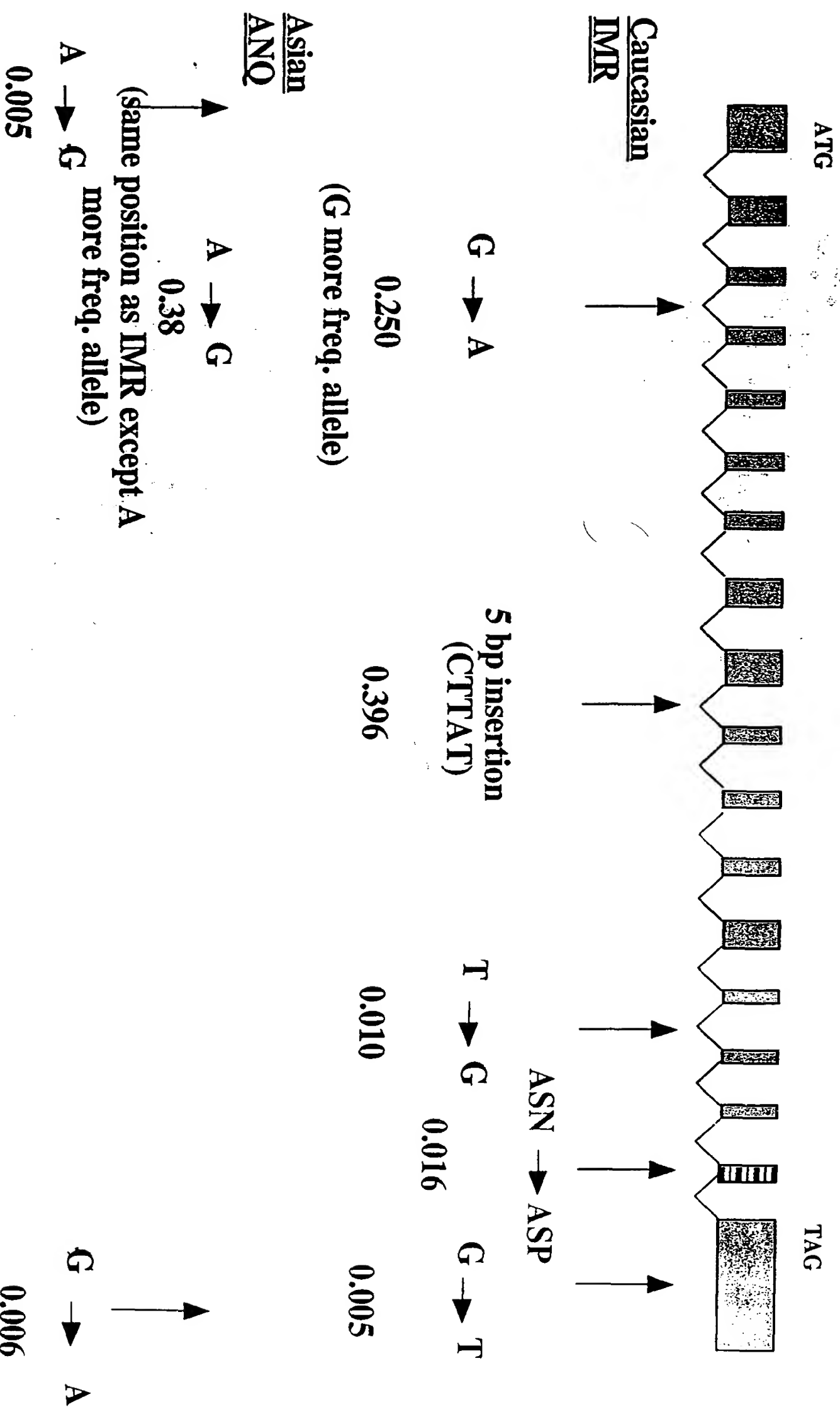


Figure 13A
09635501.080900

ACE Homologue Variants IMR and ANQ

GAATTGGGCTTCATCTCTAATACGACTCACTAATAGGGCTGAGCGGGCCCGGGGCGAGGTATCTGGCTACAGGGGACGATGTCAAG
CTCTCCTGGCTCCTTCTCAGCCTGTTGCTGTACTGCTGCTCAGTCCACCATTGAGGAACAGGCCAAGACATTTTGGACAAGTTAAC
CACGAAGCCGAAGACCCTGTTCTATCAAAAGTTCACTTGCTCTTGGAAATTATACACCATAATTACTGAAGAGAAATGTCCAAAACAT /
GAATAATGCTGGGGACAATGAGTGTGCTTTTAAAGGAACAGTCCACACTGGCC
CAATGTATCCACTACAGAAGAAATTCAGAATCTCAGAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGCTCTCAGTGTCTCAGAA
GACAGAGCAAAACGG / TGAACACAATCTAAAT
ACAATGAGCACCATCTACAGTACTGGAAAAGTTGTAAACCAGATAATCCACAAGAAATGCTTATTACTTGAACCAGG /
TTGAAATGAATAATGGCAACAGTTTAGACTACAATGAGAGGCTGGGC
TTGGAAAGCTGGAGATCTGAGGTGCGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGCTTGA AAAATGAGATGGCAAGACAA
ATC / ATTATGAGGACTATGGGATTAATGGAGAGGAG
ACTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGTGAACATACCTTTGAAGAG /
ATTAACCATTAATGACATCTTCATGCTATGTGAGGGC
AAAGTTGATGAATGCCATCTTCCTATATCAGTCCAAATGGATGCCCTCGCTCATTTGCTTGG /
TGATATGTGGGTAGATTTTGACAACAAATCTGTACTTTGACAGTTCCCTTTGGACAGAAA
CCAACATAGATGTTACTGATGCATGGTGGACCAG / GCCTGGATGCACAGAGAATATT
CAAGAGGGCCGAGAAAGTTCTTGTATCTGTTGGCTTCTTAATATGACTCAAGGATTTCTGGAAAATTCATGTCTAACGGACCAGGAAA
TGTTCAGAAAGCAGTCTGCCATCCACAGCTTGGACCTGGG /
GAAGGGCGACTTCAGGATCCTATGTGCACAAGGATGACAAATGGACAAATGGACACTTCCTG
ACAGCTCATGATGAGATGGGGCATATCCAGTATGATAGGCATATGCTGCACAACCTTTTCTGTAAGAAATGAGCTAATGAAGATT
CATGAAGCTGTGGGAAATCATGTCACTTCTTGCAAGCCACACCCTAAGCAATTTAAATCCATTGGTCTCTGTACCCGATTTTCAAGAAG
ACAATG / AACAGAAATAACTTCTGCTCAACAAGCACTCAGGATTTGGGACTCTGCCATTTACTTA
CATGTTAGAGAAGTGGAGGTGATGTGCTTTAAAGGGGAAATCCCAAGACCAAGTGAATGA AAAAGTGTGGAGATGAAG /
CGAGAGATAGTTGGGGTGTGGAACTGTGCCCATGATGAAA
CATACTGTACCCCGCATCTGTCTTCCATGTTCTAATGATTACTCATTCATTGG / ATATTACA
CAAGGACCCCTTACCAATTCAGTTTCAAGAAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCT
CTGCACAAATGTGACATCTCAAACTCTACAGAACTGAGCAAGCTGAGCAAACTG /
TTCAATATGCTGAGGCTTGA AAAATCAGAACTGAGCCCTAGCAATGGAAAATGTTGTAGAGGCAAGAACATGAATGTAAGGCCACT
GCTCAACTACTTTGAGCCCTATTACCTGGCTGA AAAGACCAAGAACAAATTTCTTTGTGGATGAGATCCGACTGAGTCC /
ATATGCAGACCAAGCATCAAGTGAGGATAAG
CCTAAATCAGCTCTTGAGATAAAGC / ATATGAATGGAACGACAATGAATGTACC
TGTTCCGATCATCTGTGTCATATGCTATGAGGCACTTTTAAAGTAA AAAATCAGATGATCTTTTTGGG /
GAGGAGATGTGCGAGTGGCTAATTTGAACCAAGAACTCTCTTAATTTCTT
GTCACTGCACCTAAAAATGTGTGATATCATCTCTAGAACTGAAGTTGAAAAGGCCATCAGG /
ATGTCCGGAGCCGTATCAATGATGTCTTCGCTGAATGACAAACAGCCTAGAGTTTCTGGG
GATACAGCCCAACACTTGGACCTCTAACCAAGCCCCCTGTTCCATATAGCTGATGTTTGGAGTTGTGATGGAGTGATAGTGGTTGG
CATGTGATCTGTATCTTCACTGGGATCAGAGATCGGAAGAAG /
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GAAAATAAATCCAGGATTCCAAAACACTGATGTTGAGACCTCTTTAGAAAATCTATGTTTCTCTTGAGGTGATTTGTGTATG
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TAAGGATTTGTATTAGAGTATATTAGGAAAGTGTGTAATTTGCTCAGAGGCTGTTGAGGATAATCTAAATGTAATGTCTGTGAATT
TCTGAAGTTGAAAACAAGATATATCATTTGAGCAAGTGTGGATCTTGTAATGGAATATGATGATGATCACTGTGAAGCAGTGCCTGG
GAACTGTGTAGCTGCAAGGATTGAGATGGCATGTCATTAAGCTTCATTTAATCAATTGTCAAGGATGACATGCTTTCTTCACAGTA
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CCGTGAACCTCCAGAGCATGTGCTGATAGAACTCAATTTCTACTGTTCTTAAGTGTGAGTGAATGGAATTTCCAAGTATGTTCACCT
CTGAAGTGGGTACCCAGTCTCTTAATCTTTTGTATTGTCTCACAGTGTGAGCAGTGTGAGCACA AAAGCAGACACTCAATAAATGCTA
GATTACACACTC / AAAAAAAAAAAAAAAAAAGGGCGGCCGC

A - G Intronic
1c/1d

G - A Intronic
A - G Intronic
3a/3b

5 bp insertion (CTTA)
Intronic
9a/9b

T - G Intronic
14a/14b

A - G ASN - ASP
17c/17d

A - G 3'UTR
18c/18d
G - T 3'UTR
18e/18f